This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Goodman, Corey S.
Kidd, Thomas
Mitchell, Kevin
Tear, Guy

(ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and Nucleic Acids

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
(B) STREET: 75 DENISE DRIVE
(C) CITY: HILLSBOROUGH
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94010

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: OSMAN, RICHARD A
(B) REGISTRATION NUMBER: 36,627
(C) REFERENCE/DOCKET NUMBER: B98-006

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 343-4341
(B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCATCCCA TGCATCCCGA AAACCACGCC ATCGCCCGGA GCACGAGCAC CACTAATAAC 60
CCATCTCGCA GTCGGAGCAG CAGGATGTGG CTCCTGCCCG CCTGGCTGCT CCTCGTCCTG 120
GTGGCCAGCA ATGGCCTGCC AGCAGTCAGA GGCCAGTACC AATCGCCACG TATCATCGAG 180
CATCCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG 240

47	GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA	300
48	AAGAAATCGC ACCGCGTCCA GTTCAAGGAC GGCGCCCTCT TCTTTTACAG GACAATGCAA	360
49	GGCAAGAAGG AGCAGGACGG CGGAGAGTAC TGGTGCGTGG CCAAGAACCG AGTGGGCCAG	420
50	GCCGTTAGTC GCCATGCCTC CCTCCAGATA GCTGTTTTGC GCGACGATTT TCGCGTGGAG	480
51	CCCAAAGACA CGCGAGTGGC CAAAGGCGAG ACGGCTCTGC TGGAGTGTGG GCCGCCCAAA	540
52	GGCATTCCAG AGCCAACGCT GATTTGGATA AAGGACGGCG TTCCCTTGGA CGACCTGAAA	600
53	GCCATGTCGT TTGGCGCCAG CTCCCGCGTT CGAATTGTGG ACGGTGGCAA CCTGCTGATC	660
54	AGCAATGTGG AGCCCATTGA TGAGGGCAAC TACAAGTGCA TTGCCCAGAA TCTGGTAGGC	720
55	ACCCGCGAGA GCAGCTATGC CAAGCTGATT GTCCAGGTCA AACCATACTT TATGAAGGAG	780
56	CCCAAGGATC AGGTGATGCT CTACGGCCAG ACAGCCACTT TCCACTGCTC AGTGGGCGGT	840
57	GATCCGCCGC CGAAAGTGTT GTGGAAAAAG GAGGAGGGCA ATATTCCGGT GTCCAGAGCG	900
58	CGAATCCTTC ACGACGAGAA AAGTTTAGAG ATATCCAACA TAACGCCCAC CGATGAGGGC	960
59	ACCTATGTCT GCGAGGCACA CAACAATGTC GGTCAGATCA GCGCTAGGGC TTCTCTTATA	1020
60	GTCCACGCTC CGCCGAACTT TACGAAAAGA CCCAGTAACA AGAAAGTGGG ACTAAATGGG	1080
61	GTTGTCCAAC TACCTTGCAT GGCCTCCGGA AACCCTCCGC CGTCTGTATT CTGGACCAAG	1140
62	GAAGGAGTAT CCACTCTTAT GTTCCCAAAT AGTTCGCACG GAAGGCAGTA TGTGGCTGCC	1200
63	GATGGAACTC TGCAGATTAC GGATGTGCGG CAGGAAGACG AAGGCTACTA TGTGTGTTCC	1260
64	GCTTTCAGTG TAGTCGATTC CTCTACAGTA CGGGTTTTCC TGCAAGTCAG CTCGGTAGAC	1320
65	GAGCGTCCAC CTCCGATTAT TCAAATCGGA CCTGCCAATC AAACACTGCC CAAGGGATCA	1380
66	GTTGCTACTT TACCCTGTCG GGCCACTGGA AATCCCAGTC CCCGTATCAA GTGGTTCCAC	1440
67	GATGGACATG CCGTACAAGC GGGCAATCGA TACAGCATCA TCCAAGGAAG CTCACTGAGA	1500
68	GTCGATGACC TTCAACTAAG TGACTCTGGT ACCTACACCT GCACTGCATC TGGCGAACGA	1560
69	GGAGAAACTT CCTGGGCTGC CACACTAACG GTGGAAAAAC CCGGTTCTAC ATCTCTTCAC	1620
70	CGGGCAGCTG ATCCTAGCAC TTATCCTGCT CCTCCAGGAA CACCTAAAGT CCTGAATGTC	1680
71	AGTCGCACCA GCATTAGTCT TCGTTGGGCT AAAAGCCAAG AGAAACCCGG AGCTGTGGGC	1740
72	CCAATCATTG GATACACTGT AGAGTACTTC AGTCCGGATC TGCAAACTGG TTGGATTGTG	1800
73	GCTGCCCATC GAGTCGGCGA CACTCAAGTC ACTATCTCGG GTCTCACTCC TGGCACTTCG	1860
74	TATGTGTTCC TAGTTAGAGC TGAGAATACT CAGGGTATTT CTGTGCCTTC CGGCTTATCA	1920
75	AATGTTATTA AAACCATTGA GGCAGATTTC GATGCAGCTT CTGCCAATGA TTTGTCAGCA	1980
76	GCTCGAACTT TGCTGACAGG AAAGTCGGTG GAGCTAATAG ATGCCTCGGC TATCAATGCT	2040
77	AGTGCCGTTA GACTTGAGTG GATGCTCCAC GTGAGCGCTG ATGAGAAATA CGTAGAGGGC	2100
78	CTGCGCATAC ACTATAAGGA TGCCAGTGTA CCATCCGCAC AGTATCACTC GATCACTGTT	2160
79	ATGGATGCCT CTGCAGAATC GTTTGTGGTG GGAAACCTTA AGAAGTACAC CAAGTATGAG	2220
80	TTCTTCCTAA CACCCTTTTT TGAGACAATT GAAGGACAGC CCAGTAACTC CAAGACAGCC	2280
81	CTCACCTATG AAGATGTTCC CTCCGCACCA CCGGATAACA TTCAGATTGG CATGTACAAC	2340
82	CAAACAGCCG GTTGGGTGCG TTGGACTCCG CCACCCTCCC AGCACCACAA TGGCAATTTG	2400
83	TATGGCTACA AGATTGAGGT CAGCGCCGGT AACACCATGA AGGTGCTGGC CAATATGACT	2460
84	CTTAATGCTA CCACCACATC TGTGCTCCTA AATAACCTAA CCACCGGAGC TGTGTACAGC	2520
85	GTGAGGTTGA ACTCCTTTAC CAAGGCAGGA GATGGACCTT ACTCCAAACC GATATCACTA	2580
86	TTCATGGACC CCACCCATCA TGTGCATCCG CCACGGGCAC ATCCAAGCGG CACCCATGAT	2640
87	GGGCGACATG AGGGACAGGA TCTCACGTAT CATAACAATG GCAACATACC ACCTGGCGAC	2700
88	ATTAATCCCA CCACTCATAA AAAGACCACT GACTACCTAT CTGGACCGTG GCTAATGGTG	2760
89	CTGGTCTGCA TCGTTCTTCT AGTCCTGGTT ATTTCGGCGG CTATTTCGAT GGTCTACTTC	2820
90	AAGCGCAAGC ATCAAATGAC CAAGGAATTG GGTCACTTAA GTGTGGTCAG TGACAACGAA	2880
91	ATAACCGCAT TAAATATCAA TAGCAAAGAG AGCCTTTGGA TAGACCATCA TCGTGGATGG	2940
92	CGAACTGCCG ATACTGACAA AGACTCAGGA TTAAGCGAAT CGAAGCTACT ATCCCACGTT	3000
93	AACAGCAGTC AATCCAACTA CAATAACTCC GATGGAGGAA CCGATTATGC AGAAGTTGAC	3060
94	ACCCGTAACC TTACCACCTT CTACAATTGT CGCAAGAGCC CCGATAATCC CACGCCGTAC	3120
95	GCCACCACTA TGATCATTGG TACCTCTTCC AGTGAGACCT GCACCAAGAC AACATCTATA	3180
96	AGTGCCGATA AGGACTCGGG AACTCATTCG CCCTATTCTG ACGCATTTGC CGGTCAGGTG	3240
97	CCAGCGGTTC CTGTTGTCAA ATCCAACTAT CTTCAGTATC CGGTTGAACC GATCAACTGG	3300
98	TCAGAGTTTC TACCCCCGCC GCCAGAACAC CCACCTCCGT CTTCTACCTA TGGATACGCA	3360
99	CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA	3420

```
AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG    3480
GGAGTATCGC CCCAATATGC TGTCGCCTGT CCACCGGAAA ACGTTTATAG CAATCCGCTG    3540
TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCCACAAA CCAACATCCG    3600
CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC    3660
CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG    3720
CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG    3780
CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCGGTGCA TCCCAATAGC    3840
CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG    3900
GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC    3960
AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG    4020
GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC    4080
TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC    4140
GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA                 4188

(2) INFORMATION FOR SEQ ID NO:2:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1395 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: peptide
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
      Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
      1               5                  10                  15
      Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
                  20                  25                  30
      Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
              35                  40                  45
      Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
          50                  55                  60
      Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
      65                  70                  75                  80
      Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
                      85                  90                  95
      Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
                  100                 105                 110
      Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
              115                 120                 125
      Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
          130                 135                 140
      His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
      145                 150                 155                 160
      Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
                      165                 170                 175
      Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
                  180                 185                 190
      Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
              195                 200                 205
      Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
          210                 215                 220
      Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
      225                 230                 235                 240
      Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
```

```
                    245                 250                 255
Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
            260                 265                 270
Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
        275                 280                 285
Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
    290                 295                 300
Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
305                 310                 315                 320
Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
                    325                 330                 335
Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
            340                 345                 350
Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
        355                 360                 365
Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
    370                 375                 380
Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
385                 390                 395                 400
Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
                    405                 410                 415
Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
            420                 425                 430
Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
        435                 440                 445
Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
    450                 455                 460
Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
465                 470                 475                 480
Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
                    485                 490                 495
Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
            500                 505                 510
Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
        515                 520                 525
Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
    530                 535                 540
Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
545                 550                 555                 560
Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
                    565                 570                 575
Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
            580                 585                 590
Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
        595                 600                 605
Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
    610                 615                 620
Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
625                 630                 635                 640
Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
                    645                 650                 655
Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
            660                 665                 670
```

```
206  Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
207          675                 680                 685
208  Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
209      690                 695                 700
210  Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
211  705                 710                 715                 720
212  Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
213                  725                 730                 735
214  Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
215              740                 745                 750
216  Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
217          755                 760                 765
218  Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
219      770                 775                 780
220  Trp Val Arg Trp Thr Pro Pro Pro Ser Gln His His Asn Gly Asn Leu
221  785                 790                 795                 800
222  Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
223                  805                 810                 815
224  Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
225              820                 825                 830
226  Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
227          835                 840                 845
228  Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
229      850                 855                 860
230  Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
231  865                 870                 875                 880
232  Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
233                  885                 890                 895
234  Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
235              900                 905                 910
236  Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
237          915                 920                 925
238  Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
239      930                 935                 940
240  Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
241  945                 950                 955                 960
242  Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
243                  965                 970                 975
244  His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
245              980                 985                 990
246  Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn
247          995                 1000                1005
248  Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu
249      1010                1015                1020
250  Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr
251  1025                1030                1035                1040
252  Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Ser Glu Thr Cys Thr Lys
253                  1045                1050                1055
254  Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr
255              1060                1065                1070
256  Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser
257          1075                1080                1085
258  Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION ***US/08/971,172***

DATE: 06/26/98
TIME: 13:36:16

INPUT SET: S27002.raw

Line	Error	Original Text